

D. Srivastava

#11 1653
7/12/99

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/962,560A

DATE: 07/13/1999
TIME: 15:32:26

INPUT SET: S32531.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Hilton, Douglas J.
Alexander, Warren S.
Viney, Elizabeth M.
Willson, Tracy A.
Richardson, Rachael T.
Starr, Robyn
Nicholson, Sandra E.
Metcalf, Donald
Nicola, Nicos A.

(ii) TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC AGENTS

(iii) NUMBER OF SEQUENCES: 50

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Scully, Scott, Murphy & Presser
(B) STREET: 400 Garden City Plaza
(C) CITY: Garden City, New York
(D) STATE: New York
(E) COUNTRY: U.S.A.
(F) ZIP: 11530

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/962,560
(B) FILING DATE: 31-OCT-1997

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/AU97/00729
(B) FILING DATE: 31-OCT-1997

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PO5117
(B) FILING DATE: 14-FEB-1997

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PO 3384

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RAW SEQUENCE LISTING
PATENT APPLICATION US/08/962,560ADATE: 07/13/1999
TIME: 15:32:27

INPUT SET: S32531.raw

47 (B) FILING DATE: 01-NOV-1996
48
49 (viii) ATTORNEY/AGENT INFORMATION:
50 (A) NAME: DiGiglio, Frank S.
51 (B) REGISTRATION NO: 31,346
52 (C) REFERENCE/DOCKET NUMBER: 10976
53

54 (ix) TELECOMMUNICATION INFORMATION:
55 (A) TELEPHONE: (516) 742-4343
56 (B) TELEFAX: (516) 742-4366
57 (C) TELEX:
58

59 (2) INFORMATION FOR SEQ ID NO:1:
60

61 (i) SEQUENCE CHARACTERISTICS:
62 (A) LENGTH: 20 base pairs
63 (B) TYPE: nucleic acid
64 (C) STRANDEDNESS: single
65 (D) TOPOLOGY: linear
66

67 (ii) MOLECULE TYPE: DNA
68

69 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
70

71 CACGCCGCC ACGTGAAGGC
72

20

73 (2) INFORMATION FOR SEQ ID NO:2:
74

75 (i) SEQUENCE CHARACTERISTICS:
76 (A) LENGTH: 20 base pairs
77 (B) TYPE: nucleic acid
78 (C) STRANDEDNESS: single
79 (D) TOPOLOGY: linear
80

81 (ii) MOLECULE TYPE: DNA
82

83 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
84

85 TTCGCCAATG ACAAGACGCT
86

20

87 (2) INFORMATION FOR SEQ ID NO:3:
88

89 (i) SEQUENCE CHARACTERISTICS:
90 (A) LENGTH: 1235 base pairs
91 (B) TYPE: nucleic acid
92 (C) STRANDEDNESS: single
93 (D) TOPOLOGY: linear
94

95 (ii) MOLECULE TYPE: DNA
96

97 (ix) FEATURE:
98

98 (A) NAME/KEY: CDS
99 (B) LOCATION: 161..799

RAW SEQUENCE LISTING PATENT APPLICATION US/08/962,560A

DATE: 07/13/1999

TIME: 15:32:27

INPUT SET: S32531.raw

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101      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
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103      CGAGGCTCAA GCTCCGGGCG GATTCTGCGT GCCGCTCTCG CTCCTTGGGG TCTGTTGGCC      60
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105      GGCCTGTGCC ACCCGGACGC CCGGCTCACT GCCTCTGTCT CCCCATCAG CGCAGCCCCG      120
106
107      GACGCTATGG CCCACCCCTC CAGCTGGCCC CTCGAGTAGG      160
108
109      ATG GTA GCA CGC AAC CAG GTG GCA GCC GAC AAT GCG ATC TCC CCG GCA      208
110      Met Val Ala Arg Asn Gln Val Ala Ala Asp Asn Ala Ile Ser Pro Ala
111      1          5          10          15
112
113      GCA GAG CCC CGA CGG CGG TCA GAG CCC TCC TCG TCC TCG TCT TCG TCC      256
114      Ala Glu Pro Arg Arg Arg Ser Glu Pro Ser Ser Ser Ser Ser Ser Ser
115      20          25          30
116
117      TCG CCA GCG GCC CCC GTG CGT CCC CGG CCC TGC CCG GCG GTC CCA GCC      304
118      Ser Pro Ala Ala Pro Val Arg Pro Arg Pro Cys Pro Ala Val Pro Ala
119      35          40          45
120
121      CCA GCC CCT GGC GAC ACT CAC TTC CGC ACC TTC CGC TCC CAC TCC GAT      352
122      Pro Ala Pro Gly Asp Thr His Phe Arg Thr Phe Arg Ser His Ser Asp
123      50          55          60
124
125      TAC CGG CGC ATC ACG CGG ACC AGC GCG CTC CTG GAC GCC TGC GGC TTC      400
126      Tyr Arg Arg Ile Thr Arg Thr Ser Ala Leu Leu Asp Ala Cys Gly Phe
127      65          70          75          80
128
129      TAT TGG GGA CCC CTG AGC GTG CAC GGG GCG CAC GAG CGG CTG CGT GCC      448
130      Tyr Trp Gly Pro Leu Ser Val His Gly Ala His Glu Arg Leu Arg Ala
131      85          90          95
132
133      GAG CCC GTG GGC ACC TTC TTG GTG CGC GAC AGT CGT CAA CGG AAC TGC      496
134      Glu Pro Val Gly Thr Phe Leu Val Arg Asp Ser Arg Gln Arg Asn Cys
135      100          105          110
136
137      TTC TTC GCG CTC AGC GTG AAG ATG GCT TCG GGC CCC ACG AGC ATC CGC      544
138      Phe Phe Ala Leu Ser Val Lys Met Ala Ser Gly Pro Thr Ser Ile Arg
139      115          120          125
140
141      GTG CAC TTC CAG GCC GGC CGC TTC CAC TTG GAC GGC AGC CGC GAG ACC      592
142      Val His Phe Gln Ala Gly Arg Phe His Leu Asp Gly Ser Arg Glu Thr
143      130          135          140
144
145      TTC GAC TGC CTT TTC GAG CTG CTG GAG CAC TAC GTG GCG GCG CCG CGC      640
146      Phe Asp Cys Leu Phe Glu Leu Leu Glu His Tyr Val Ala Ala Pro Arg
147      145          150          155          160
148
149      CGC ATG TTG GGG GCC CCG CTG CGC CAG CGC CGC GTG CGG CCG CTG CAG      688
150      Arg Met Leu Gly Ala Pro Leu Arg Gln Arg Arg Val Arg Pro Leu Gln
151      165          170          175
152

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RAW SEQUENCE LISTING PATENT APPLICATION US/08/962,560A

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153 GAG CTG TGT CGC CAG CGC ATC GTG GCC GCC GTG GGT CGC GAG AAC CTG      736
154 Glu Leu Cys Arg Gln Arg Ile Val Ala Ala Val Gly Arg Glu Asn Leu
155           180           185           190
156 GCG CGC ATC CCT CTT AAC CCG GTA CTC CGT GAC TAC CTG AGT TCC TTC      784
157 Ala Arg Ile Pro Leu Asn Pro Val Leu Arg Asp Tyr Leu Ser Ser Phe
158           195           200           205
159
160 CCC TTC CAG ATC TGA CCGGCTG CCGCTGTGCC GCAGCATTAAGTGGGGGCGC      836
161 Pro Phe Gln Ile
162           210
163
164 CTTATTATTT CTTATTATTA ATTATTATTA TTTTCTGGA ACCACGTGGG AGCCCTCCCC      896
165
166 GCCTGGGTCG GAGGGAGTGG TTGTGGAGGG TGAGATGCCT CCCACTTCTG GCTGGAGACC      956
167
168 TCATCCCACC TCTCAGGGGT GGGGGTGCTC CCCTCCTGGT GCTCCCTCCG GGTCCCCCCT      1016
169
170 GGTGTAGCA GCTGTGTCT GGGGCCAGGA CCTGAATTCC ACTCCTACCT CTCCATGTTT      1076
171
172 ACATATTCCC AGTATCTTTG CACAAACCAG GGGTCGGGGA GGGTCTCTGG CTTCAATTTT      1136
173
174 CTGCTGTGCA GAATATCCTA TTTTATATTT TTACAGCCAG TTAGGTAAT AAACCTTTATT      1196
175
176 ATGAAAGTTT TTTTAAATAA GAAAAAAAAA AAAAAAAAAA      1235
177
178 (2) INFORMATION FOR SEQ ID NO:4:
179
180 (i) SEQUENCE CHARACTERISTICS:
181 (A) LENGTH: 212 amino acids
182 (B) TYPE: amino acid
183 (D) TOPOLOGY: linear
184
185 (ii) MOLECULE TYPE: protein
186
187 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
188
189 Met Val Ala Arg Asn Gln Val Ala Ala Asp Asn Ala Ile Ser Pro Ala
190 1 5 10 15
191
192 Ala Glu Pro Arg Arg Arg Ser Glu Pro Ser Ser Ser Ser Ser Ser
193 20 25 30
194
195 Ser Pro Ala Ala Pro Val Arg Pro Arg Pro Cys Pro Ala Val Pro Ala
196 35 40 45
197
198 Pro Ala Pro Gly Asp Thr His Phe Arg Thr Phe Arg Ser His Ser Asp
199 50 55 60
200
201 Tyr Arg Arg Ile Thr Arg Thr Ser Ala Leu Leu Asp Ala Cys Gly Phe
202 65 70 75 80
203
204 Tyr Trp Gly Pro Leu Ser Val His Gly Ala His Glu Arg Leu Arg Ala
205 85 90 95

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INPUT SET: S32531.raw

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206  Glu Pro Val Gly Thr Phe Leu Val Arg Asp Ser Arg Gln Arg Asn Cys
207              100                      105                      110
208
209  Phe Phe Ala Leu Ser Val Lys Met Ala Ser Gly Pro Thr Ser Ile Arg
210              115                      120                      125
211
212  Val His Phe Gln Ala Gly Arg Phe His Leu Asp Gly Ser Arg Glu Thr
213              130                      135                      140
214
215  Phe Asp Cys Leu Phe Glu Leu Leu Glu His Tyr Val Ala Ala Pro Arg
216              145                      150                      155                      160
217
218  Arg Met Leu Gly Ala Pro Leu Arg Gln Arg Arg Val Arg Pro Leu Gln
219              165                      170                      175
220
221  Glu Leu Cys Arg Gln Arg Ile Val Ala Ala Val Gly Arg Glu Asn Leu
222              180                      185                      190
223
224  Ala Arg Ile Pro Leu Asn Pro Val Leu Arg Asp Tyr Leu Ser Ser Phe
225              195                      200                      205
226
227  Pro Phe Gln Ile
228              210
229
230
231  (2) INFORMATION FOR SEQ ID NO:5:
232
233      (i) SEQUENCE CHARACTERISTICS:
234          (A) LENGTH: 1121 base pairs
235          (B) TYPE: nucleic acid
236          (C) STRANDEDNESS: single
237          (D) TOPOLOGY: linear
238
239      (ii) MOLECULE TYPE: DNA
240
241      (ix) FEATURE:
242          (A) NAME/KEY: CDS
243          (B) LOCATION: 223..819
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245      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
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247  GCGATCTGTG GGTGACAGTG TCTGCGAGAG ACTTTGCCAC ACCATTCTGC CGGAATTTGG      60
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249  AGAAAAAGAA CCAGCCGCTT CCAGTCCCCT CCCCTCCGC CACCATTTCG GACACCCTGC      120
250
251  ACACCTCTCGT TTTGGGGTAC CCTGTGACTT CCAGGCAGCA CGCGAGGTCC ACTGGCCCCA      180
252
253  GCTCGGGCGA CCAGCTGTCT GGGACGTGTT GACTCATCTC CC ATG ACC CTG CGG      234
254                      Met Thr Leu Arg
255                      1
256
257
258  TGC CTG GAG CCC TCC GGG AAT GGA GCG GAC AGG ACG CGG AGC CAG TGG      282

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PAGE: 1

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PATENT APPLICATION US/08/962,560A

DATE: 07/13/1999
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